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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=3; day=26; hr=10; min=17; sec=4; ms=180;]

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Reviewer Comments:

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo
Tadanori Mayumi
Yasuo Tsutsumi
Shinsaku Nakagawa

In the second to fourth applicant lines, please use this format:
Surname, First Name (example: Mayumi, Tadanori).

<210> 1
<211> 157
<212> PRT
<213> human

<400>

Please change the <213> response to "Homo sapiens". Per Section 1.823 of the Sequence Rules, use "Genus species". Please insert a "1" on the <400> line (e.g, <400> 1)

<210> 2
<211> 471
<212> DNA
<213> Artificial Sequence

<400> 2

gtc aga tca tct tct cga acc ccg agt gac atg cct gta gcc cat gtt 48
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
1 5 10 15
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96

Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg		
			20					25					30				
gcc	aat	gcc	ctc	ctg	gcc	aat	ggc	gtg	gag	ctg	aga	gat	aac	cag	ctg	144	
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu		
		35					40					45					
gtg	gtg	cca	tca	gag	ggc	ctg	tac	ctc	atc	tac	tcc	cag	gtc	ctc	ttc	192	
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe		
	50					55				60							
tcg	ggc	caa	ggc	tgc	ccc	tcc	acc	cat	gtg	ctc	ctc	acc	cac	acc	atc	240	
Ser	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile		
65					70					75					80		
agc	cgc	atc	gcc	gtc	tcc	tac	cag	acc	ccc	gtc	aac	ctc	ctc	tct	gcc	288	
Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Pro	Val	Asn	Leu	Leu	Ser	Ala		
			85					90				95					
atc	cgc	agc	ccc	tgc	cag	agg	gag	acc	cca	gag	ggg	gct	gag	gcc	aac	336	
Ile	Arg	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Asn		
			100					105				110					
ccc	tgg	tat	gag	ccc	atc	tat	ctg	gga	ggg	gtc	ttc	cag	ctg	gag	ccg	384	
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Pro		
		115					120					125					
ggt	gac	cga	ctc	agc	gct	gag	atc	aat	cgg	ccc	gac	tat	ctc	gac	ttt	432	
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe		
	130					135					140						
gcc	gag	tct	ggg	cag	gtc	tac	ttt	ggg	atc	att	gcc	ctg					
Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu					
145					150					155							

Per 1.823 of the Sequence Rules: if the <213> response is either "Artificial Sequence" or "Unknown", please insert a <220>-<223> section explaining the source of the genetic material. Please insert a cumulative total of "471" at the right margin of the last nucleotide above. These two types of errors appear in many subsequent sequences. Please correct them.

<210> 5
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<400> 5
 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
 1 5 10 15

Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Xaa	Asn	Xaa	Xaa
			20					25					30		
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu
		35					40					45			
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe
	50					55					60				
Ser	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile
65					70					75					80
Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Pro	Val	Asn	Leu	Leu	Ser	Ala
				85					90					95	
Ile	Arg	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Asn
			100					105					110		
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Pro
	115						120					125			
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe
	130					135					140				
Xaa	Xaa	Xaa	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu			
145					150					155					

Please: 1) insert a <220>-<223> section explaining "Artificial Sequence"; 2) please explain all Xaa's in a separate <220>-<223> section (which amino acids do they represent?). These two types of errors appear in many subsequent sequences.

<210> 6

<211> 471

<212> DNA

<213> Artificial Sequence

<400> 6

gtc	aga	tca	tct	tct	cga	acc	ccg	agt	gac	atg	cct	gta	gcc	cat	gtt	48
Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Met	Pro	Val	Ala	His	Val	
1				5				10				15				
gta	gca	aac	cct	caa	gct	gag	ggg	cag	ctc	cag	tgg	nns	aac	nns	nns	96
Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Xaa	Asn	Xaa	Xaa	
		20						25				30				
gcc	aat	gcc	ctc	ctg	gcc	aat	ggc	gtg	gag	ctg	aga	gat	aac	cag	ctg	144
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	
	35						40					45				
gtg	gtg	cca	tca	gag	ggc	ctg	tac	ctc	atc	tac	tcc	cag	gtc	ctc	ttc	192
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	

50	55	60	
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc	240		
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile			
65	70	75	80
agc cgc atc gcc gtc tcc tac cag acc ccc gtc aac ctc ctc tct gcc	288		
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala			
85	90	95	
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac	336		
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn			
100	105	110	
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg	384		
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro			
115	120	125	
ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt	432		
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe			
130	135	140	
nns nns nns ggg cag gtc tac ttt ggg atc att gcc ctg			
Xaa Xaa Xaa Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu			
145	150	155	

Please: 1) explain "Artificial Sequence"; 2) explain all "n's" in a separate <220>-<223> section; which nucleotides do they represent? 3) please insert a cumulative nucleotide total of "471" at the right margin of the last nucleotide line. These three types of errors appear in many subsequent sequences.

```
<210> 9
<211> 157
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Clone No.5
```

As an explanation of "Artificial Sequence", the above <223> response needs more information regarding its source. Same error in many subsequent sequences.

```
<210> 83
<211> 87
<212> DNA
<213> Artificial Sequence
```

<220>

<223> Oligonucleotide as a primer having NNS sequences (for mutating the amino acid residues at the 29,31 and 32)

<400> 83

gacatgcctg tagcccatgt tgtagcaaac cctcaagctg aggggcagct ccagtgggns 60
aacnnsnsg ccaatgccct cctggcc

The above <223> response exceeds the Sequence Rules' required 72-character line limit; insert a hard return.

Please explain all n's in a separate <220>-<223> section. Please insert a cumulative nucleotide total at the right margin of the last nucleotide line. Same errors in subsequent sequences.

<210> 84

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide as a primer having NNS sequences (for mutating the amino acid residues at the 145 to 147)

<400> 84

cagggcaatg atcccaaagt agacctgcc s nnsnnsnna aagtcgagat agtcggg

Please insert a hard return in the <223> response; please correct spelling of "residues" (not "resudues"). What is "at the 145 to 147"? Please explain all n's. Please insert a cumulative nucleotide total at the right margin of the nucleotide line. These errors appear in subsequent sequences.

Please ensure that all subsequent sequences follow the directions above. Suggestion: please consult the Sequence Rules for valid format.

Application No: 10585296 Version No: 1.0

Input Set:**Output Set:**

Started: 2010-03-16 10:24:54.294
Finished: 2010-03-16 10:25:08.538
Elapsed: 0 hr(s) 0 min(s) 14 sec(s) 244 ms
Total Warnings: 90
Total Errors: 130
No. of SeqIDs Defined: 90
Actual SeqID Count: 90

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
E 201	Mandatory field data missing in <400> SEQID: (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 341	'Xaa' position not defined SEQID (5) POS (29)
E 341	'Xaa' position not defined SEQID (5) POS (31)
E 341	'Xaa' position not defined SEQID (5) POS (32)

Input Set:

Output Set:

Started: 2010-03-16 10:24:54.294
Finished: 2010-03-16 10:25:08.538
Elapsed: 0 hr(s) 0 min(s) 14 sec(s) 244 ms
Total Warnings: 90
Total Errors: 130
No. of SeqIDs Defined: 90
Actual SeqID Count: 90

Error code	Error Description
E 341	'Xaa' position not defined SEQID (5) POS (145)
E 341	'Xaa' position not defined SEQID (5) POS (146)
E 341	'Xaa' position not defined SEQID (5) POS (147)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 342	'n' position not defined found at POS: 85 SEQID(6)
E 342	'n' position not defined found at POS: 86 SEQID(6)
E 342	'n' position not defined found at POS: 91 SEQID(6)
E 342	'n' position not defined found at POS: 92 SEQID(6)
E 342	'n' position not defined found at POS: 94 SEQID(6)
E 342	'n' position not defined found at POS: 95 SEQID(6)
E 341	'Xaa' position not defined SEQID (6) POS (29)
E 341	'Xaa' position not defined SEQID (6) POS (31)
E 341	'Xaa' position not defined SEQID (6) POS (32)
E 342	'n' position not defined found at POS: 433 SEQID(6)
E 342	'n' position not defined found at POS: 434 SEQID(6)
E 342	'n' position not defined found at POS: 436 SEQID(6)
E 342	'n' position not defined found at POS: 437 SEQID(6)
E 342	'n' position not defined found at POS: 439 SEQID(6)
E 342	'n' position not defined found at POS: 440 SEQID(6)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(6)

Input Set:

Output Set:

Started: 2010-03-16 10:24:54.294
Finished: 2010-03-16 10:25:08.538
Elapsed: 0 hr(s) 0 min(s) 14 sec(s) 244 ms
Total Warnings: 90
Total Errors: 130
No. of SeqIDs Defined: 90
Actual SeqID Count: 90

Error code	Error Description
E 341	'Xaa' position not defined SEQID (6) POS (145)
E 341	'Xaa' position not defined SEQID (6) POS (146)
E 341	'Xaa' position not defined SEQID (6) POS (147)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E 341	'Xaa' position not defined SEQID (7) POS (84)
E 341	'Xaa' position not defined SEQID (7) POS (85)
E 341	'Xaa' position not defined SEQID (7) POS (86)
E 341	'Xaa' position not defined SEQID (7) POS (87)
E 341	'Xaa' position not defined SEQID (7) POS (88)
E 341	'Xaa' position not defined SEQID (7) POS (89)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E 342	'n' position not defined found at POS: 250 SEQID(8)
E 342	'n' position not defined found at POS: 251 SEQID(8)
E 342	'n' position not defined found at POS: 253 SEQID(8)
E 342	'n' position not defined found at POS: 254 SEQID(8)
E 342	'n' position not defined found at POS: 256 SEQID(8)
E 342	'n' position not defined found at POS: 257 SEQID(8)
E 342	'n' position not defined found at POS: 259 SEQID(8)
E 342	'n' position not defined found at POS: 260 SEQID(8)

This error has occurred more than 20 times, will not be displayed

Input Set:

Output Set:

Started: 2010-03-16 10:24:54.294
Finished: 2010-03-16 10:25:08.538
Elapsed: 0 hr(s) 0 min(s) 14 sec(s) 244 ms
Total Warnings: 90
Total Errors: 130
No. of SeqIDs Defined: 90
Actual SeqID Count: 90

Error code	Error Description
E 341	'Xaa' position not defined SEQID (8) POS (84)
E 341	'Xaa' position not defined SEQID (8) POS (85) This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(23)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 441 SEQID(24)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(25)

Input Set:

Output Set:

Started: 2010-03-16 10:24:54.294
Finished: 2010-03-16 10:25:08.538
Elapsed: 0 hr(s) 0 min(s) 14 sec(s) 244 ms
Total Warnings: 90
Total Errors: 130
No. of SeqIDs Defined: 90
Actual SeqID Count: 90

Error code	Error Description
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(26)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(27)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(28)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(29)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(30)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(31)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(32)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(33)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(34)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(35)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(36)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(60)

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo
 Tadanori Mayumi
 Yasuo Tsutsumi
 Shinsaku Nakagawa

<120> TNF antagonist and TNF inhibitor containing it as an effective ingredient

<130> WO1042

<140> 10585296

<141> 2010-03-16

<160> 90

<210> 1

<211> 157

<212> PRT

<213> human

<400>

Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val
1				5					10					15	
Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg
			20					25					30		
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu
			35					40					45		
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe
			50					55				60			
Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile
					70					75					80
Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala
					85					90					95
Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys
			100						105				110		
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys
			115						120				125		
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe
			130					135				140			
Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu			
145					150					155					

<210> 2

<211> 471

<212> DNA

<213> Artificial Sequence

<400> 2

gtc	aga	tca	tct	tct	cga	acc	ccg	agt	gac	atg	cct	gta	gcc	cat	gtt	48
Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Met	Pro	Val	Ala	His	Val	
1				5					10					15		
gta	gca	aac	cct	caa	gct	gag	ggg	cag	ctc	cag	tgg	ctg	aac	cgc	cgg	96
Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	
				20					25				30			
gcc	aat	gcc	ctc	ctg	gcc	aat	ggc	gtg	gag	ctg	aga	gat	aac	cag	ctg	144

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
agc cgc atc gcc gtc tcc tac cag acc ccc gtc aac ctc ctc tct gcc 288
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala
85 90 95
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac 336
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
100 105 110
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg 384
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
115 120 125
ggg gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 3
<211> 471
<212> DNA
<213> Artificial Sequence

<400> 3
gtc aga tca tct tct cga acc ccg agt gac gcg cct gta gcc cat gtt 48
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Ala Pro Val Ala His Val
1 5 10 15
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
20 25 30
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg 144
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
agc cgc atc gcc gtc tcc tac cag acc cgg gtc aac ctc ctc tct gcc 288
Ser Arg Ile Ala Val Ser Tyr Gln Thr Arg Val Asn Leu Leu Ser Ala
85 90 95
atc gcc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc ctc 336
Ile Ala Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Leu
100 105 110
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag acc 384
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Thr
115 120 125
ggg gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe

130 135 140
 gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg
 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 145 150 155

<210> 4
 <211> 471
 <212> DNA
 <213> Artificial Sequence

<400> 4
 gtc aga tca tct tct cga acc ccg agt gac gcg cct gta gcc cat gtt 48
 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Ala Pro Val Ala His Val
 1 5 10 15
 gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96
 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 20 25 30
 gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg 144
 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 35 40 45
 gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192
 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
 50 55 60
 tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240
 Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
 65 70 75 80
 agc cgc atc gcc gtc tcc tac cag acc gac gtc aac ctc ctc tct gcc 288
 Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala
 85 90 95
 atc gcc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc ctc 336
 Ile Ala Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Leu
 100 105 110
 ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag acc 384
 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Thr
 115 120 125
 ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432
 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
 130 135 140
 gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg
 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 145 150 155

<210> 5
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<400> 5
 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
 1 5 10 15
 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Xaa Asn Xaa Xaa
 20 25 30
 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 35 40 45
 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe

50		55		60	
Ser Gly Gln Gly Cys Pro	Ser Thr His Val Leu Leu Thr His Thr Ile				
65	70	75	80		
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala					
85	90	95			
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn					
100	105	110			
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro					
115	120	125			
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe					
130	135	140			
Xaa Xaa Xaa Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu					
145	150	155			

<210> 6

<211> 471

<212> DNA

<213> Artificial Sequence

<400> 6

gtc aga tca tct tct cga acc ccg agt gac atg cct gta gcc cat gtt	48		
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val			
1	5	10	15
gta gca aac cct caa gct gag ggg cag ctc cag tgg nns aac nns nns	96		
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Xaa Asn Xaa Xaa			
20	25	30	
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg	144		
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu			
35	40	45	
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc	192		
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe			
50	55	60	
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc	240		
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile			
65	70	75	80
agc cgc atc gcc gtc tcc tac cag acc ccc gtc aac ctc ctc tct gcc	288		
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala			
85	90	95	
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac	336		
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn			
100	105	110	
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg	384		
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro			
115	120	125	
ggg gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt	432		
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe			
130	135	140	
nns nns nns ggg cag gtc tac ttt ggg atc att gcc ctg			
Xaa Xaa Xaa Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu			
145	150	155	

<210> 7

<211> 157

<212> PRT

<213> Artificial Sequence

<400> 7

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Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
  1              5              10              15
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
              20              25              30
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
              35              40              45
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
              50              55              60
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
              65              70              75              80
Ser Arg Ile Xaa Xaa Xaa Xaa Xaa Xaa Pro Val Asn Leu Leu Ser Ala
              85              90              95
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
              100             105             110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
              115             120             125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
              130             135             140
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145              150              155
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<210> 8

<211> 471

<212> DNA

<213> Artificial Sequence

<400> 8

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gtc aga tca tct tct cga acc ccg agt gac atg cct gta gcc cat gtt 48
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
  1              5              10              15
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
              20              25              30
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg 144
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
              35              40              45
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
              50              55              60
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
              65              70              75              80
agc cgc atc nns nns nns nns nns nns ccc gtc aac ctc ctc tct gcc 288
Ser Arg Ile Xaa Xaa Xaa Xaa Xaa Xaa Pro Val Asn Leu Leu Ser Ala
              85              90              95
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac 336
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
              100             105             110
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg 384
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
              115             120             125
ggg gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
              130             135             140
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gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 9
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone No.5

<400> 9
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
1 5 10 15
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Arg Asn Ser His
20 25 30
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala
85 90 95
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
100 105 110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
115 120 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
Ser Gly Thr Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 10
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone No.6

<400> 10
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
1 5 10 15
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Ser Asn Arg Tyr
20 25 30
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala
85 90 95

Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
100 105 110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
115 120 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
Ser Met
145

<210> 11
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone No.7

<400> 11
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
1 5 10 15
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp His Asn Asn Thr
20 25 30
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala
85 90 95
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
100 105 110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
115 120 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
Asp Ser Asn Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 12
<211> 157
<212> PRT
<213> Artifici